ABSTRACT

A method is provided for identifying multiple different activated transcription factors in a cell sample. The method includes transducing or transfecting a cell sample with a library of constructs. In one embodiment, each construct includes a different cis element sequence to which a specific transcription factor is known to bind, a promoter sequence 3' relative to the cis element sequence, and a different reporter sequence 3' relative to the promoter sequence. Upon binding of a transcription factor to one of the cis elements, the reporter sequence is transcribed. Determination of the transcribed reporter sequence identifies the cis element contained in the same construct as the reporter sequence, thereby identifying the corresponding transcription factor that binds to the cis element. The method can be used for efficiently detecting activation of multiple different transcription factors in a cell sample.